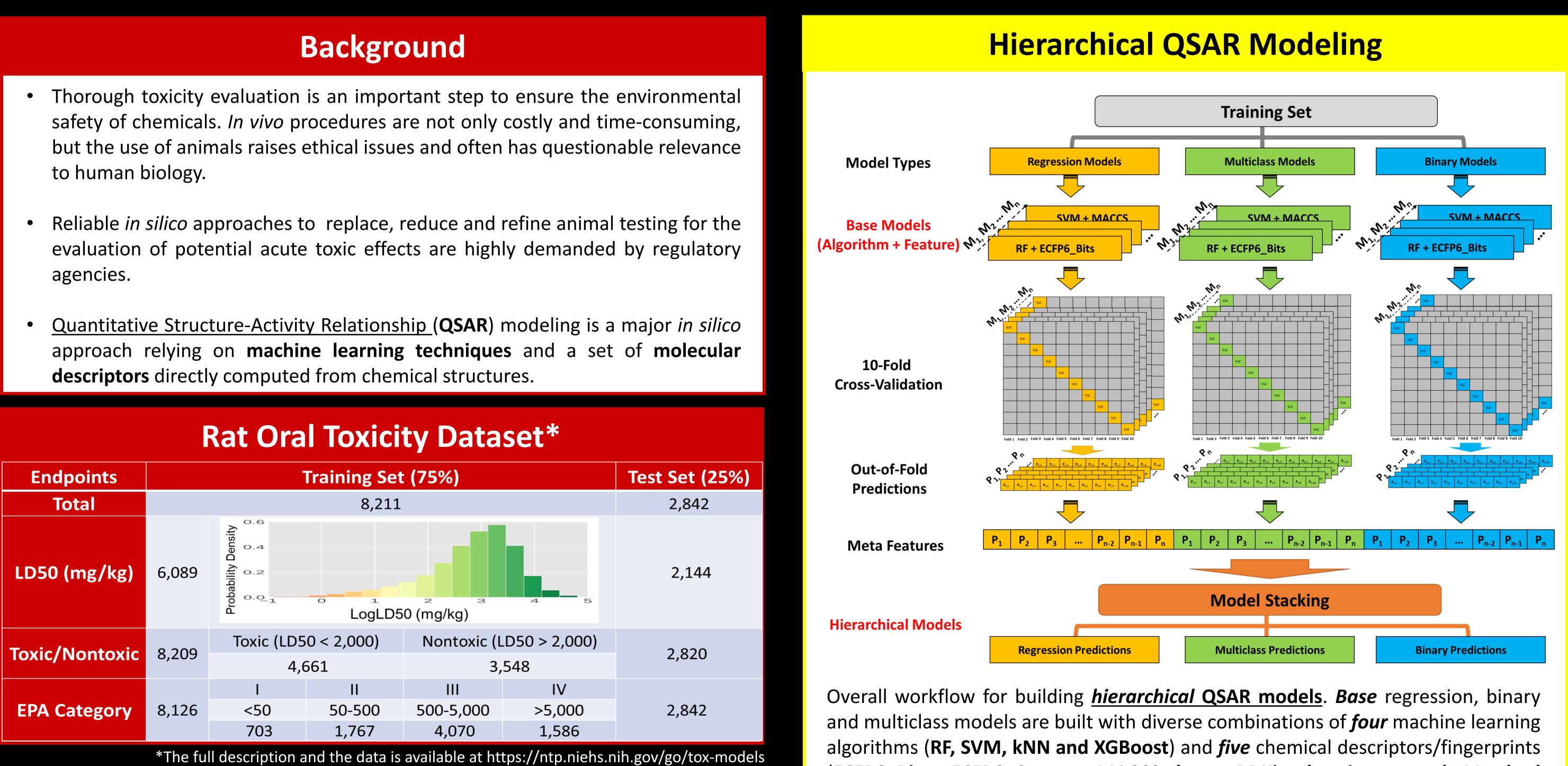
NC STATE UNIVERSITY

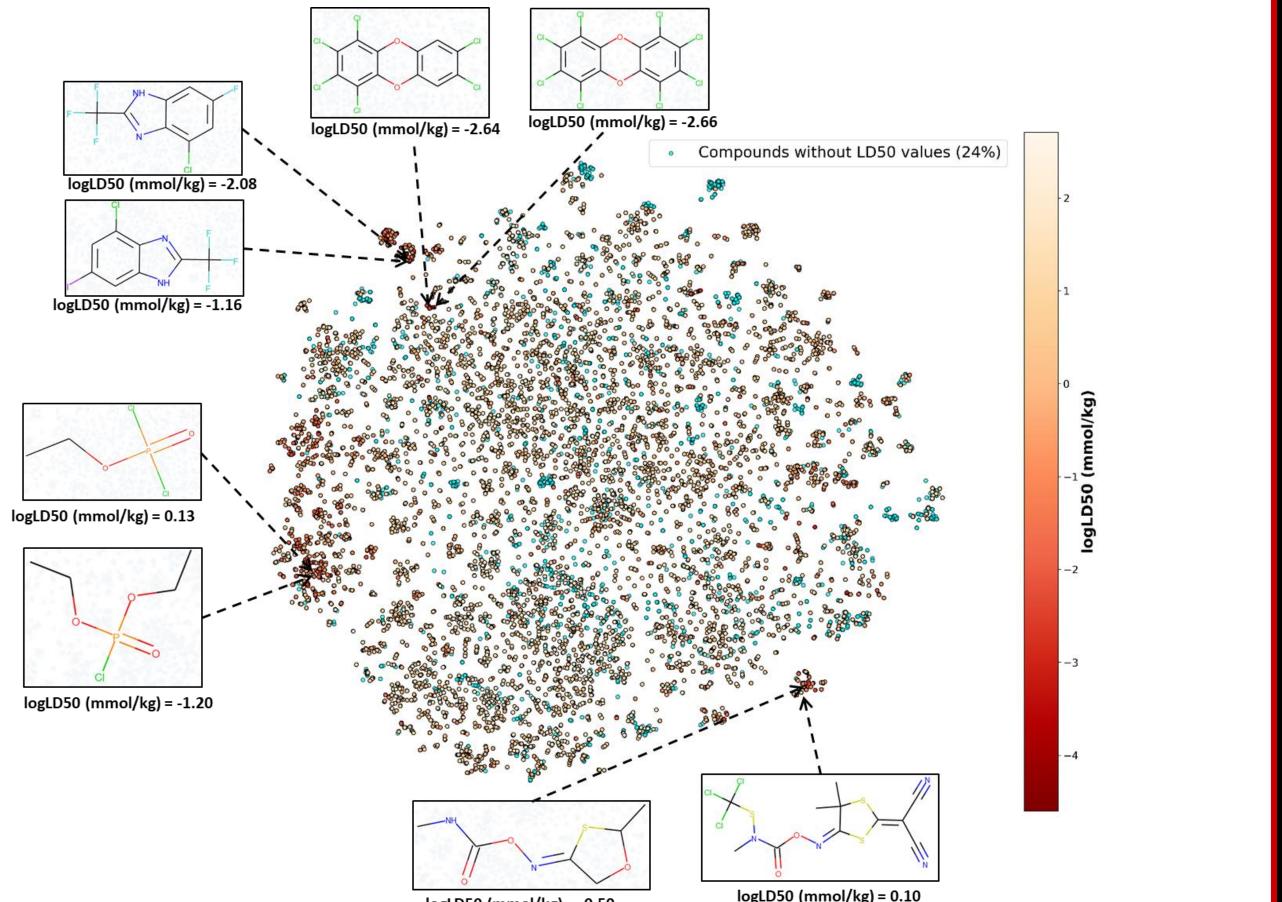


¹ Department of Chemistry, Bioinformatics Research Center, North Carolina State University, Raleigh, NC 27695, United States ² National Toxicology Program Interagency Center for the Evaluation of Alternative Toxicological Methods, NIEHS, RTP, North Carolina 27709, United States.

- to human biology.
- agencies.
- **descriptors** directly computed from chemical structures.



Visualization of the Chemical Space

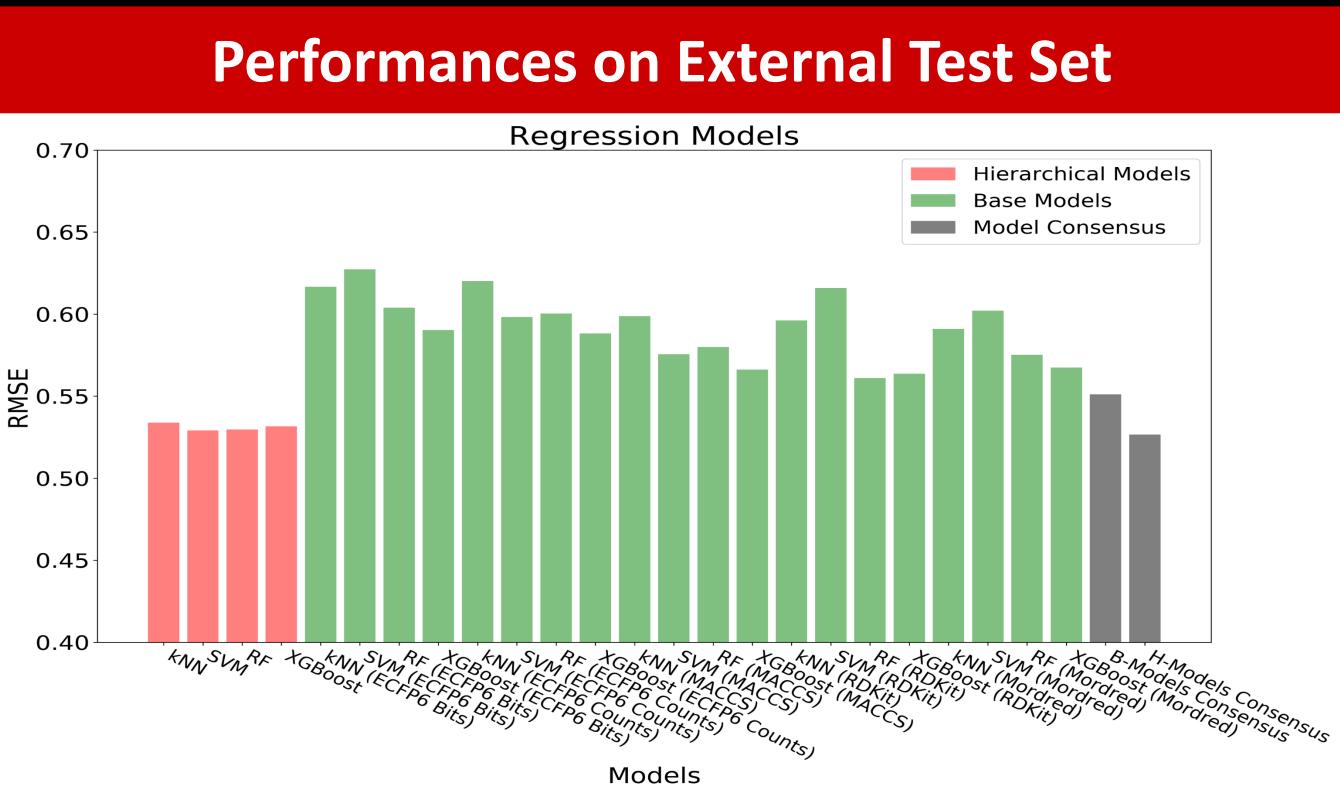


Clustering of the full dataset (11,056 molecules) by t-SNE with 2D bit-based ECFP6 (2,048 bits)

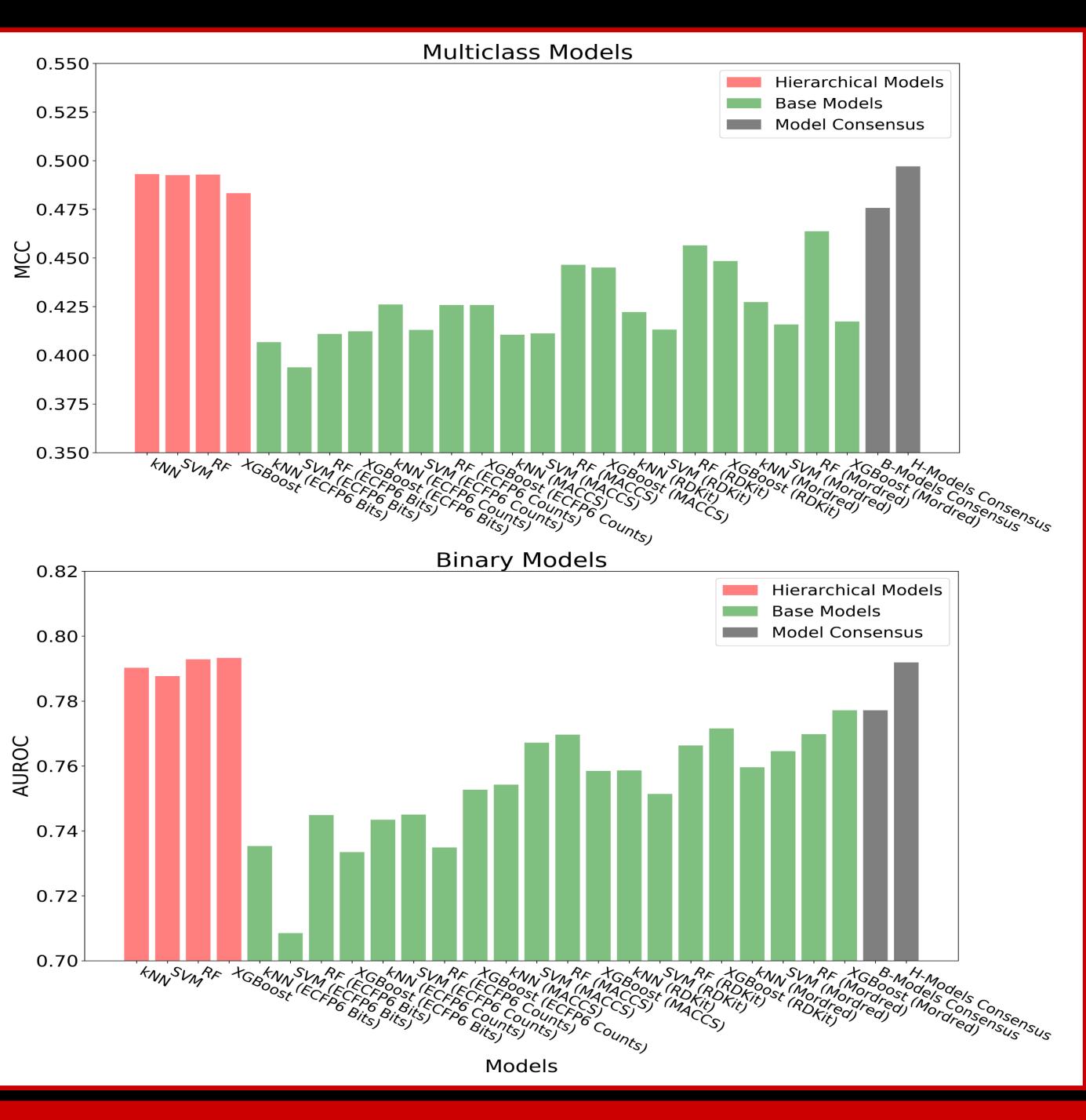
Hierarchical QSAR Modeling for Predicting Acute Oral Systemic Toxicity

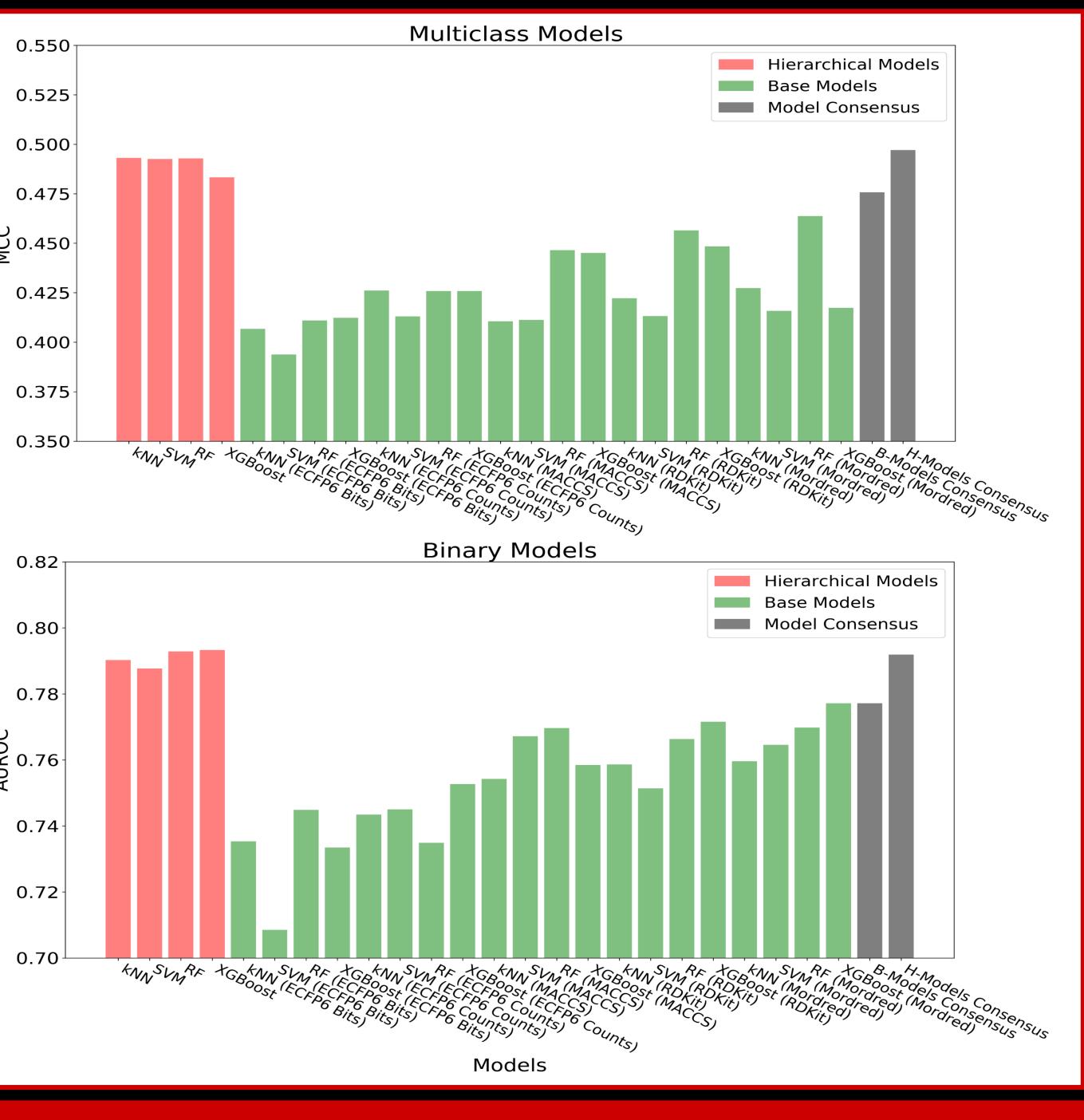
Xinhao Li¹, Nicole C. Kleinstreuer², and Denis Fourches^{1,*}

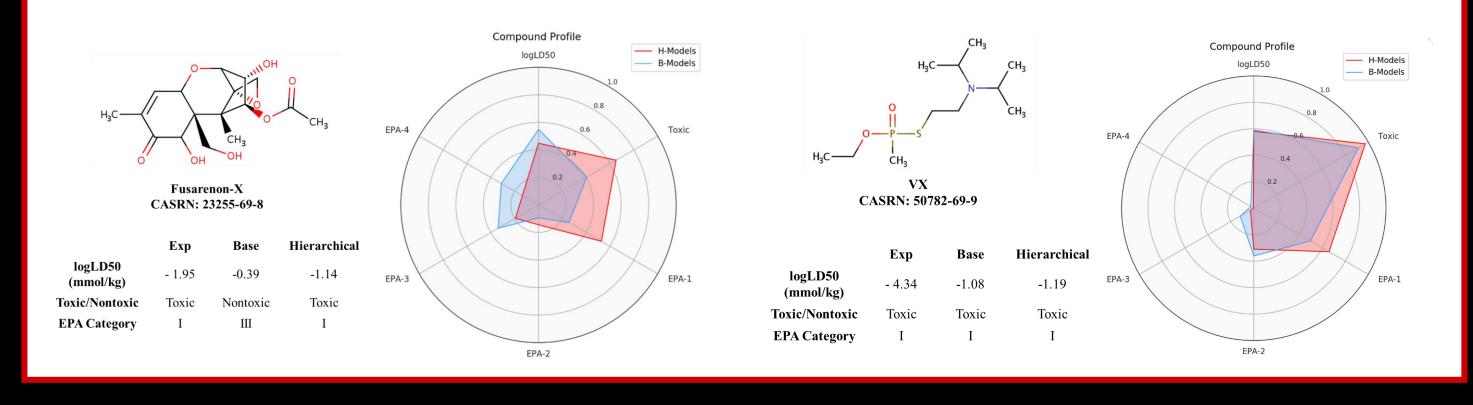
binary and multiclass models.



(ECFP6_Bits, ECFP6_Counts, MACCS keys, RDKit descriptors and Mordred descriptors). For each endpoint, a diverse set of 20 models were built at this stage (60 base models total). Out-of-Fold Predictions of base models are generated through 10-fold cross-validation. The out-of-fold predictions are concatenated together and used as input (Meta Features) for building hierarchical regression,







- the individual base models on all the three endpoints.

Examples of Chemicals in External Test Set

Conclusion

A dual-layer hierarchical QSAR modeling protocol was developed and applied to three acute oral systemic toxicity endpoints. The hierarchical models outperform

Hierarchical H-QSAR modeling method relying on the full stacking of binary, multiclass, and regression models represents a promising approach for in silico chemical risk assessment and more generally, for blending individual QSAR models

Acknowledgement

NC State Chancellor's Faculty Excellence Program, NIEHS, CHHE.